

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Jeffrey E. Russell Examiner #: 62-785 Date: 10-15-2002
 Art Unit: 1654 Phone Number 308-5775 Serial Number: 09/208,832
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL
CM1-11009 / CM1-9807

If more than one search is submitted, please prioritize searches in order of need. MEJ

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Peptidase-cleavable, targeted antineoplastic drugs and their therapeutic use
 Inventors (please provide full names): R. Copeland, C. Albright, A. Conds, R. Dowling, N. Gresigni,
W. Han, C. Hogle, P. Huang, E. Yue, S. DiMeo
 Earliest Priority Filing Date: 3-13-2001

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 186 (XPLGXYL) in STN,

in the U.S. patent application sequence database (issued & pending),
 and in Genesys/Subsynd/PTR. Please require any hits to have
 10 or fewer residues.

Thank you.

JER

Point of Contact
 Mona Smith
 Technical Information Specialist
 CM1 6A01
 Tel: 308-3778

Russell
 09/208,832
 ID 186
 10/15/02

STAFF USE ONLY

Searcher: in Su
 Searcher Phone #: _____
 Searcher Location: _____
 Date Searcher Picked Up: 10/15/02
 Date Completed: 10/24/02
 Searcher Prep & Review Time: 1.0
 Clerical Prep Time: _____
 Online Time: 15

Type of Search

NA Sequence (#) _____
 AA Sequence (#) 1
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr. Link _____
 Lexis/Nexis _____
 Sequence Systems _____
 WWW/Internet _____
 Other (specify) _____

=> fil hcaplu
FILE 'HCAPLUS' ENTERED AT 13:09:09 ON 23 OCT 2002
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PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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FILE COVERS 1907 - 23 Oct 2002 VOL 137 ISS 17
FILE LAST UPDATED: 22 Oct 2002 (20021022/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

=> d stat que
L1 4 SEA FILE=REGISTRY XPLGXYL/SQSP
L2 371099 SEA FILE=REGISTRY SQL=<10
L3 4 SEA FILE=REGISTRY L1 AND L2
L4 1 SEA FILE=HCAPLUS L3

=> d ibib abs hitrn 14

L4 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:693138 HCAPLUS
DOCUMENT NUMBER: 135:273218
TITLE: Preparation of peptidase-cleavable, targeted antineoplastic drugs and their therapeutic use
INVENTOR(S): Copeland, Robert A.; Albright, Charles F.; Combs, Andrew P.; Dowling, Radine L.; Graciani, Nilsa R.; Han, Wei; Higley, C. Anne; Huang, Pearl S.; Yue, Eddy W.; Dimeo, Susan V.
PATENT ASSIGNEE(S): Dupont Pharmaceuticals Company, USA
SOURCE: PCT Int. Appl., 203 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001068145	A2	20010920	WO 2001-US8589	20010315
WO 2001068145	A3	20020711		
W: AT, AU, BR, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, HU, IN, JP, KR, LT, LU, LV, MX, NZ, PL, PT, RO, RU, SE, SG, SI, SK, UA, VN, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
US 2002103133	A1	20020801	US 2001-808832	20010315
PRIORITY APPLN. INFO.:			US 2000-189387P P 20000315	
OTHER SOURCE(S):		MARPAT 135:273218		
AB	This invention is directed to antineoplastic agents conjugated to enzyme-cleavable peptides comprising the amino acid recognition sequence of a membrane-bound and/or cell-secreted peptidase. The conjugated compds. are for use as chemotherapeutic agents in the targeted treatment of cancers. Claimed peptide sequences include Cap-Paa-Xa2-Gly-Xpl-Laa, where Cap is an N-terminus group R, Xa4 or R-Xa4 (R is an amino capping group, Xa4 is an amino acid), Paa is Pro, 4-hydroxyproline (Hyp), 2-carboxyazetidine (Aze), homo-Pro, cyclohexylglycine (Chg), 4-fluorophenylalanine (Fph), nipecotic acid (Npa), 4-thiazolidinecarboxylic acid (Tzc), or proline mimetic; Xa2 is an amino acid; Xpl is is an amino acid wherein -Gly-Xpl- or -Sar-Xpl form a bond cleavable by a matrixin; Laa is an amino acid, e.g., Leu, Ile, Nle, .beta.-homo-Leu, homoleucine, homoserine, Ala and cyclohexylalanine. Thus, peptide conjugate Ac-PLGLYL-Dox (Dox = doxorubicin) was prepd. by the solid phase method and evaluated for stability in blood and cleavage with MMPs and neprilysin.			
IT	360780-48-9P RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) (prepn. of antineoplastic agents conjugated to enzyme-cleavable peptides)			
IT	362675-79-4 362676-88-8 362677-10-9 RL: PRP (Properties) (unclaimed protein sequence; prepn. of peptidase-cleavable, targeted antineoplastic drugs and their therapeutic use)			

=> fil reg

FILE 'REGISTRY' ENTERED AT 13:09:34 ON 23 OCT 2002

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Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 22 OCT 2002 HIGHEST RN 464152-74-7

DICTIONARY FILE UPDATES: 22 OCT 2002 HIGHEST RN 464152-74-7

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> s l4

L5 4 L3

=> d rn cn lc nte sql kwic can tot l5

L5 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2002 ACS
RN 362677-10-9 REGISTRY
CN 185: PN: W00168145 SEQID: 186 unclaimed protein (9CI) (CA INDEX NAME)
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL
NTE

type	location	description
uncommon	Aaa-1	-
uncommon	Aaa-5	-

SQL 7

SQL 7

SEQ 1 XPLGXLYL

=====

HITS AT: 1-7

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:273218

L5 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2002 ACS
RN 362676-88-8 REGISTRY
CN 175: PN: W00168145 SEQID: 176 unclaimed protein (9CI) (CA INDEX NAME)
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL
NTE

type	location	description
uncommon	Aaa-1	-
uncommon	Aaa-5	-

SQL 7

SQL 7

SEQ 1 XPLGXLYL

=====

HITS AT: 1-7

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:273218

L5 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2002 ACS
 RN 362675-79-4 REGISTRY
 CN 104: PN: W00168145 SEQID: 105 unclaimed protein (9CI) (CA INDEX NAME)
 LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL
 NTE

type	location	description
uncommon	Aaa-1	-
uncommon	Aaa-5	-

SQL 7

SQL 7

SEQ 1 XPLGXLYL

=====

HITS AT: 1-7

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:273218

L5 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2002 ACS
 RN 360780-48-9 REGISTRY
 CN 5,12-Naphthacenedione, 10-[[3-[[N-acetyl-L-.gamma.-glutamyl-L-prolyl-L-leucylglycyl-.alpha.-aminobenzenebutanoyl-L-tyrosyl-L-leucyl)amino]-2,3,6-trideoxy-.alpha.-L-lyxo-hexopyranosyl]oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-, (8S,10S)- (9CI) (CA INDEX NAME)
 LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL
 NTE modified (modifications unspecified)

type	location	description
uncommon	Ggu-1	-
uncommon	Aaa-5	-

SQL 7

SQL 7

SEQ 1 XPLGXLYL

=====

HITS AT: 1-7

REFERENCE 1: 135:273218

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 13:41:42 ; Search time 30 Seconds
(without alignments)
25.917 Million cell updates/sec

Title: US-09-808-832-186
Perfect score: 30
Sequence: 1 XPLGXYL 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 135323

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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 21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
 22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
<hr/>							
1	23	76.7	6	22	AAU07722	Human matrix type-	
2	23	76.7	8	19	AAW52141	Matrix metalloprot	
3	23	76.7	8	22	AAB97518	Substituted phosph	
4	23	76.7	10	21	AAB51837	Human secreted pro	
5	23	76.7	10	22	AAB97519	Substituted phosph	
6	22	73.3	9	20	AAV48081	Immunogenic peptid	
7	21	70.0	8	19	AAW54885	Isozyme-specific a	
8	21	70.0	9	20	AAV48098	Immunogenic peptid	
9	21	70.0	9	22	AAU06336	Human Leukocyte An	
10	21	70.0	10	20	AAV46811	Immunogenic peptid	
11	20	66.7	10	22	AAG96570	Human complementar	
12	19	63.3	6	18	AAW28950	Opioid peptide. S	
13	19	63.3	6	18	AAW24311	New peptide which	
14	19	63.3	6	20	AAV23060	Opioid peptide whi	
15	19	63.3	7	6	AAP50083	Thiopeptolide havi	
16	19	63.3	8	20	AAW89344	Peptide SEQ ID NO:	
17	19	63.3	10	15	AAR61665	Peptide fragment (
18	18	60.0	6	21	AAB37325	Peptide linker #10	
19	18	60.0	6	21	AAB15681	Matrix metalloprot	
20	18	60.0	6	21	AAB22834	Matrix metalloprot	
21	18	60.0	6	21	AAB01558	Collagenase substr	
22	18	60.0	6	22	AAU07359	Metalloproteinase	
23	18	60.0	6	22	AAB67721	Amino acid sequenc	
24	18	60.0	6	22	AAB67722	Amino acid sequenc	
25	18	60.0	6	22	AAB73911	MMP-2 protease cle	
26	18	60.0	6	22	AAB73912	MT1-MMP protease c	
27	18	60.0	6	22	AAB35976	Collagenase cleava	
28	18	60.0	7	15	AAR67143	Enkephalin derived	

29	18	60.0	7	17	AAR87156	Variant bovine gro
30	18	60.0	7	18	AAW24983	Recombinant human
31	18	60.0	7	22	AAG65041	Human matrix metal
32	18	60.0	7	22	AAB75135	Gelatinase recogni
33	18	60.0	7	22	AAB74039	Synthetic collagen
34	18	60.0	7	22	AAB35980	Gelatinase cleavab
35	18	60.0	8	14	AAR35857	Hepatitis C virus
36	18	60.0	8	14	AAR35858	Hepatitis C virus
37	18	60.0	8	14	AAR35859	Hepatitis C virus
38	18	60.0	8	14	AAR35860	Hepatitis C virus
39	18	60.0	8	16	AAR73431	Human TSH receptor
40	18	60.0	8	16	AAR73432	Human TSH receptor
41	18	60.0	8	19	AAY20465	Human microtubule
42	18	60.0	8	22	AAB97545	Substituted phosph
43	18	60.0	8	22	AAB62230	MMP substrate octa
44	18	60.0	8	22	AAB86845	MMP-2 and MMP-9 bi
45	18	60.0	9	15	AAY38358	PAP-derived HLA-bi

ALIGNMENTS

RESULT 1

AAU07722

ID AAU07722 standard; peptide; 6 AA.

XX

AC AAU07722;

XX

DT 21-NOV-2001 (first entry)

XX

DE Human matrix type-1-metalloprotease protease cleavage site.

XX

KW Human matrix type-1-metalloprotease; MT1-MMP;

KW protease cleavage site; cytostatic; antirheumatic;

KW antirheumatic; antiarthritic; immunosuppressive; antiinflammatory;

KW anti-HIV; virucide; viral display; gene therapy; cancer; inflammation;

KW rheumatoid arthritis; autoimmune disease; infection; AIDS;

KW acquired immunodeficiency syndrome; herpes; hepatitis;

KW protease inhibitor; drug screening.

XX

OS Homo sapiens.

XX

PN WO200162980-A1.

XX

PD 30-AUG-2001.

XX

PF 23-FEB-2001; 2001WO-US05859.

XX

PR 25-FEB-2000; 2000US-0185203.

XX

PA (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.

XX

PI Russell SJ, Chadwick MP;

XX

DR WPI; 2001-541706/60.

XX

PT Identifying protease inhibitors by assaying for the presence of a

PT transferable label from a viral display package in the presence of test

PT compound, where an increase in cell label indicates the compound as a

PT protease inhibitor -

XX

PS Example 1; Page 20; 46pp; English.

XX

CC The invention relates to identifying a test substance for the ability to

CC inhibit a protease by contacting a protease-containing target cell with a

CC viral display package (comprising a receptor-binding polypeptide which

CC binds to a receptor on the surface of the cell, a protease cleavage site

CC for the protease expressed by the cell, and a fusion-mediating

CC polypeptide, such that proteolytic cleavage of the cleavage site does not

CC permit substantial transfer of the transferable label from the phage

CC package to the cell), and detecting a transferable label to indicate if

CC the substance is a protease inhibitor. The method is useful for

CC identifying a test substance for its ability to inhibit a protease. The

CC delivery of an expressible polynucleotide to a target cell is also

CC possible, and both methods are applicable for a number of target cells.

CC The methods are useful for therapeutic purposes and as a model system for

CC optimising delivery of transferable labels. The protease inhibitors

CC identified are useful for treating cancer, inflammation, rheumatoid

CC arthritis, autoimmune diseases, infections including AIDS (acquired

CC immunodeficiency syndrome), herpes and hepatitis. A whole range of

CC proteins, peptides, antisense transcripts and ribozyme sequences can be

CC encoded within an expressible polynucleotide (i.e. a gene therapy

CC technique) and delivered to a target cell for a therapeutic effect. The

CC target cells may also be cells infected by pathogens such as HIV virus,

CC rhinovirus, herpes virus, hepatitis virus or other infectious agents

CC which expresses proteases. The present sequence is a human matrix type-1-

CC metalloprotease (MT1-MMP) protease cleavage site which may be used as a

CC component of the viral display package used in the method of the

CC invention.

XX

SQ Sequence 6 AA;

Query Match 76.7%; Score 23; DB 22; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLGXY 6

|||

Db 1 PLGLY 5

RESULT 2

AAW52141

ID AAW52141 standard; Peptide; 8 AA.

XX

AC AAW52141;

XX

DT 20-JUL-1998 (first entry)

XX

DE Matrix metalloproteinase MMP-9 substrate MR1.

XX

KW Membrane-type matrix metalloproteinase; MT-MMP; MT1-MMP;

KW matrix metalloproteinase 12; MMP-12; osteoclastic proteinase;

KW osteoclast; inhibitor; metabolic bone disease; osteoporosis;

KW bone resorption; metastasis; tumour; cancer; ulcer; arthritis;

KW periodontal disease; therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Abz-glycine"

FT Cleavage-site 4..5

FT Modified-site 6

FT /note= "Norleucine"

FT Modified-site 9

FT /note= "tyrosine(NO2)"

XX

PN WO9804287-A1.

XX

PD 05-FEB-1998.

XX

PF 29-JUL-1997; 97WO-EP04110.

XX

PR 30-JUL-1996; 96GB-0015976.

XX

PA (CLIN-) CENT CLINICAL & BASIC RES.

XX

PI Delaisse J, Foged NT, Meldal M;

XX

DR WPI; 1998-130425/12.

XX

PT Use of inhibitors of protease(s) involved in osteoclast activity -

PT useful for, e.g. treating metabolic bone disease such as

PT osteoporosis

XX

PS Example 6b; Page 44; 110pp; English.

XX

CC Peptide MR1 is a substrate of matrix metalloproteinase MMP-9. Novel

CC peptide substrate mimicking MMP-inhibitors (see AAW52132-33) are

CC promising agents for use in treatment of bone metabolic disease.

CC They can be used to inhibit proteinases involved in the

CC recruitment, proliferation, differentiation or migration of

CC osteoclast precursor cells or in the migration, fusion, attachment,

CC polarisation, removal of mineralised osseous substance or death of

CC osteoclasts. The inhibitors reduce the rate of bone resorption

CC and are used to treat or prevent, e.g. osteoporosis and osteolytic

CC bone metastases. They are also useful in, e.g. treatment of

CC cancer, ulcers, arthritis and periodontal disease.

XX

SQ Sequence 8 AA;

Query Match 76.7%; Score 23; DB 19; Length 8;

Best Local Similarity 80.0%; Pred. No. 6.4e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLGXY 6

||| |

Db 2 PLGLY 6

Search completed: October 23, 2002, 13:42:22

Job time : 32 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:41:43 ; Search time 24 Seconds
(without alignments)
50.457 Million cell updates/sec

Title: US-09-808-832-186
Perfect score: 30
Sequence: 1 XPLGXLYL 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB	ID	Description
	No.	Score	Match	Length			
1	17	56.7	10	10	Q9S905		Q9s905 glycine max
2	16	53.3	8	12	Q89498		Q89498 murine hepa
3	15	50.0	10	10	Q94IS6		Q94is6 pinus taeda
4	14	46.7	8	12	Q83349		Q83349 murine coro
5	13	43.3	8	4	Q9P0K3		Q9p0k3 homo sapien
6	13	43.3	9	11	Q9QWT0		Q9qwt0 mus musculu
7	13	43.3	10	4	O60912		O60912 homo sapien
8	12	40.0	8	2	Q9RQ49		Q9rq49 buchnera ap
9	12	40.0	8	4	Q96RN9		Q96rn9 homo sapien
10	12	40.0	8	8	P92422		P92422 psathyrosta
11	12	40.0	8	8	P92373		P92373 haynaldia v
12	12	40.0	8	8	P93985		P93985 aegilops co
13	12	40.0	8	8	P92404		P92404 lophopyrum
14	12	40.0	8	8	P92426		P92426 pseudoroegn
15	12	40.0	8	8	P93973		P93973 eremopyrum
16	12	40.0	8	8	P93970		P93970 eremopyrum
17	12	40.0	8	8	P92388		P92388 henrardia p
18	12	40.0	8	8	P92428		P92428 peridictyon
19	12	40.0	8	8	P92391		P92391 heteranthel
20	12	40.0	8	8	P92227		P92227 crithopsis
21	12	40.0	8	8	P93963		P93963 psathyrosta
22	12	40.0	8	8	P93961		P93961 psathyrosta
23	12	40.0	8	8	P92215		P92215 amblyopyrum
24	12	40.0	8	8	P93981		P93981 crithodium
25	12	40.0	8	8	P92431		P92431 aegilops ta
26	12	40.0	8	8	P92222		P92222 bromus iner
27	12	40.0	8	8	P92443		P92443 taeniatheru
28	12	40.0	8	8	P92382		P92382 hordeum bra
29	12	40.0	8	8	P92384		P92384 hordeum mur
30	12	40.0	8	8	P92386		P92386 hordeum mar
31	12	40.0	8	8	P92394		P92394 hordeum vul
32	12	40.0	8	8	P93965		P93965 secale stri
33	12	40.0	8	8	P93966		P93966 aegilops sp

34	12	40.0	8	8	P92219	P92219 australopyr
35	12	40.0	8	8	P93992	P93992 australopyr
36	12	40.0	8	8	P92441	P92441 thinopyrum
37	12	40.0	8	8	P93955	P93955 festucopsis
38	12	40.0	8	8	P92211	P92211 agropyron c
39	12	40.0	8	8	P93959	P93959 hordeum ere
40	12	40.0	8	8	P93957	P93957 festucopsis
41	12	40.0	9	13	P83057	P83057 bombina var
42	12	40.0	9	13	P83056	P83056 bombina var
43	12	40.0	10	2	Q9AE19	Q9ae19 streptococc
44	12	40.0	10	4	Q9H1I5	Q9h1i5 homo sapien
45	12	40.0	10	4	Q14096	Q14096 homo sapien

ALIGNMENTS

RESULT 1

Q9S905

ID Q9S905 PRELIMINARY; PRT; 10 AA.

AC Q9S905;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE S3 PEPTIDE.

OS Glycine max (Soybean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

OX NCBI_TaxID=3847;

RN [1]

RP SEQUENCE.

RX MEDLINE=92232221; PubMed=1368037;

RA Hirano H., Kagawa H., Okubo K.;

RL Phytochemistry 31:731-735(1992).

SQ SEQUENCE 10 AA; 975 MW; 3C733271A879D1B7 CRC64;

Query Match 56.7%; Score 17; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLG 4

|||

Db 8 PLG 10

Search completed: October 23, 2002, 13:43:10

Job time : 25 secs

OM protein - protein search, using sw model

Run on: October 23, 2002, 13:41:42 ; Search time 10 Seconds
(without alignments)
27.104 Million cell updates/sec

Title: US-09-808-832-186
Perfect score: 30
Sequence: 1 XPLGXYL 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 349

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Score	Match	Length	DB ID		
No.							
1	17	56.7	9	1	OXYA_SQUAC	P42999	squalus aca
2	17	56.7	9	1	OXYT_RABIT	P32878	oryctolagus
3	17	56.7	9	1	TKL1_LOCM1	P16223	locusta mig
4	16	53.3	8	1	UF06_MOUSE	P38644	mus musculu
5	15	50.0	9	1	ISOT_CYPCA	P42993	cyprinus ca

6	15	50.0	9	1	OXYT_BUFRE	P42995	bufo regula
7	15	50.0	9	1	OXYT_OCTVU	P80027	octopus vul
8	14	46.7	7	1	FAR5_HIRME	P42564	hirudo medi
9	14	46.7	9	1	OXYA_SCYCA	P42996	scyliorhinu
10	14	46.7	9	1	OXYF_SCYCA	P42997	scyliorhinu
11	14	46.7	9	1	OXYV_SQUAC	P43000	squalus aca
12	13	43.3	10	1	TKL2_LOCFMI	P16224	locusta mig
13	12	40.0	8	1	AL17_CARMA	P81820	carcinus ma
14	12	40.0	9	1	AL11_CARMA	P81814	carcinus ma
15	12	40.0	9	1	NEUU_CAVPO	P34966	cavia porce
16	12	40.0	9	1	OXYT_EISFO	P42998	eisenia foe
17	12	40.0	9	1	TKC1_CALVO	P41517	calliphora
18	12	40.0	10	1	AMPN_HELAM	P81731	helicoverpa
19	12	40.0	10	1	CU30_LOCFMI	P11735	locusta mig
20	12	40.0	10	1	ESTA_SCHGA	P81012	schizaphis
21	12	40.0	10	1	RLA2_MOUSE	P99027	mus musculu
22	12	40.0	10	1	TKL3_LOCFMI	P30249	locusta mig
23	11	36.7	4	1	FAR3_HIRME	P42562	hirudo medi
24	11	36.7	5	1	PRCT_PERAM	P01373	periplaneta
25	11	36.7	6	1	VP19_HSV1K	P23210	herpes simp
26	11	36.7	7	1	FAR2_ASCSU	P31890	ascaris suu
27	11	36.7	7	1	GFRP_MOUSE	P99025	mus musculu
28	11	36.7	7	1	MNP1_LEPDE	P42984	leptinotars
29	11	36.7	8	1	AL15_CARMA	P81818	carcinus ma
30	11	36.7	8	1	AL16_CARMA	P81819	carcinus ma
31	11	36.7	8	1	ALL6_CYPDO	P82157	cydia pomon
32	11	36.7	8	1	ALL8_CARMA	P81811	carcinus ma
33	11	36.7	8	1	ALL9_CARMA	P81812	carcinus ma
34	11	36.7	9	1	CONO_CONGE	P05486	conus geogr
35	11	36.7	9	1	CONO_CONST	P05487	conus stria
36	11	36.7	9	1	DNF1_LOCFMI	P16339	locusta mig
37	11	36.7	9	1	FAR9_ASCSU	P43172	ascaris suu
38	11	36.7	9	1	LITO_LITAU	P08945	litoria aur
39	11	36.7	9	1	OXYT_CYPCA	P23879	cyprinus ca
40	11	36.7	9	1	OXYT_RAJCL	P42994	raja clavat
41	11	36.7	9	1	TRP4_LEUMA	P81736	leucophaea
42	11	36.7	9	1	UPA3_HUMAN	P30089	homo sapien
43	11	36.7	10	1	AL19_CARMA	P81822	carcinus ma
44	11	36.7	10	1	ANG1_BOTJA	Q10581	bothrops ja
45	11	36.7	10	1	BRK_ONCMY	Q9prz1	oncorhynchu

ALIGNMENTS

RESULT 1

OXYA_SQUAC

ID OXYA_SQUAC STANDARD; PRT; 9 AA.

AC P42999;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Aspartocin (Aspartocin).

OS Squalus acanthias (Spiny dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.

OX NCBI_TaxID=7797;

RN [1]

RP SEQUENCE.

RX MEDLINE=73031727; PubMed=5083097;

RA Acher R., Chauvet J., Chauvet M.-T.;

RT "Phylogeny of the neurohypophysial hormones. Two new active peptides

RT isolated from a cartilaginous fish, Squalus acanthias.";

RL Eur. J. Biochem. 29:12-19(1972).

RN [2]

RP SEQUENCE.

RX MEDLINE=72128038; PubMed=4622083;

RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;

RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-

RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the

RT spiny dog-fish (Squalus acanthias).";

RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR InterPro; IPR000981; Neurhypophys_horm.

DR Pfam; PF00220; hormone4; 1.

DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.

FT DISULFID 1 6

FT MOD_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 56.7%; Score 17; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLG 4

|||

Db 7 PLG 9

Search completed: October 23, 2002, 13:42:39

Job time : 12 secs

OM protein - protein search, using sw model

Run on: October 23, 2002, 13:41:47 ; Search time 14 Seconds
(without alignments)
48.045 Million cell updates/sec

Title: US-09-808-832-186
Perfect score: 30
Sequence: 1 XPLGXYL 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1099

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB ID	Description
	1	17	56.7	4	2 A32039	tyrosine-melanocyt

2	17	56.7	8 4	I54017	granulocyte-colony
3	17	56.7	9 2	A91466	oxytocin - hippopo
4	17	56.7	9 2	A92774	oxytocin - spotted
5	17	56.7	9 2	A93147	oxytocin - finback
6	17	56.7	9 2	A93408	oxytocin - Austral
7	17	56.7	9 2	B90667	oxytocin - rabbit
8	16	53.3	8 2	PT0311	Ig heavy chain CRD
9	15	50.0	8 2	PT0368	Ig gamma chain C r
10	15	50.0	9 2	A61364	isotocin - common
11	14	46.7	7 2	A11483	aspartate transami
12	13	43.3	9 2	S15850	vitamin D3 26-mono
13	13	43.3	9 2	S36850	Ig heavy chain V r
14	13	43.3	9 2	G41946	T-cell receptor ga
15	13	43.3	10 2	PT0038	glutathione transf
16	12	40.0	5 2	B61445	Leu-enkephalin - b
17	12	40.0	6 2	JN0861	peptidyl-dipeptida
18	12	40.0	8 2	PT0530	T-cell receptor be
19	12	40.0	9 2	S63491	dissimilatory sulf
20	12	40.0	9 2	S36898	ribosomal protein
21	12	40.0	9 2	PC2021	oxytocin-related p
22	12	40.0	9 2	PH1591	Ig H chain V-D-J r
23	12	40.0	10 1	ECLQ1M	tachykinin I - mig
24	12	40.0	10 1	ECLQ3M	tachykinin III - m
25	12	40.0	10 2	A43405	6-phosphofructo-2-
26	12	40.0	10 2	A60410	beta-neoendorphin
27	12	40.0	10 2	H60588	sperm-activating p
28	12	40.0	10 2	PT0243	Ig heavy chain CRD
29	12	40.0	10 2	PH1633	Ig H chain V-D-J r
30	12	40.0	10 2	PT0215	T-cell receptor be
31	12	40.0	10 2	PH0944	T-cell receptor be
32	12	40.0	10 2	PH0926	T-cell receptor be
33	12	40.0	10 2	A59173	nuclease Bh1 (EC 3
34	11	36.7	5 1	HOROHA	proctolin - Americ
35	11	36.7	5 2	A60411	proctolin - Atlant
36	11	36.7	6 2	B44510	hypothetical prote
37	11	36.7	7 2	S42407	gramicidin S synth
38	11	36.7	7 2	S78024	ribosomal protein
39	11	36.7	7 2	I48105	dihydrofolate redu
40	11	36.7	7 2	I48086	DNA topoisomerase
41	11	36.7	7 2	PD0029	pev-kinin 1 - pena
42	11	36.7	7 4	S15597	orf 4 rara 5'-regi
43	11	36.7	8 2	G33098	205K exoantigen -
44	11	36.7	8 2	S10783	enamelin f - bovin
45	11	36.7	8 2	A35180	neutral proteinase

ALIGNMENTS

RESULT 1

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C;Accession: A32039

R;Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 from bovine brain tissue.

A;Reference number: A32039; MUID:89123285

A;Accession: A32039

A;Molecule type: protein

A;Residues: 1-4 <HOR>

A;Experimental source: brain

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end

F;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 56.7%; Score 17; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLG 4

|||

Db 2 PLG 4

Search completed: October 23, 2002, 13:43:51

Job time : 15 secs

OM protein - protein search, using sw model

Run on: October 23, 2002, 13:41:47 ; Search time 13 Seconds
 (without alignments)
 13.152 Million cell updates/sec

Title: US-09-808-832-186
Perfect score: 30
Sequence: 1 XPLGXLYL 7

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 70601

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA.*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	%	
Result	Query	
No.	Score Match Length DB ID	Description

1	21	70.0	8 4	US-08-953-033-7	Sequence 7, Appli
2	19	63.3	5 2	US-08-350-260A-321	Sequence 321, App
3	19	63.3	6 1	US-08-487-006-80	Sequence 80, Appl
4	19	63.3	6 2	US-08-488-659A-80	Sequence 80, Appl
5	18	60.0	6 4	US-09-208-684-12	Sequence 12, Appl
6	18	60.0	6 4	US-09-561-500-24	Sequence 24, Appl
7	18	60.0	6 4	US-09-561-108-24	Sequence 24, Appl
8	18	60.0	7 1	US-08-340-045-16	Sequence 16, Appl
9	18	60.0	7 2	US-08-934-222-136	Sequence 136, App
10	18	60.0	7 2	US-08-933-402-136	Sequence 136, App
11	18	60.0	7 2	US-09-207-621-136	Sequence 136, App
12	18	60.0	7 2	US-08-532-818-136	Sequence 136, App
13	18	60.0	7 3	US-08-871-302A-16	Sequence 16, Appl
14	18	60.0	7 3	US-09-231-797-136	Sequence 136, App
15	18	60.0	7 3	US-08-934-224-136	Sequence 136, App
16	18	60.0	7 3	US-08-933-843-136	Sequence 136, App
17	18	60.0	7 4	US-08-934-223-136	Sequence 136, App
18	18	60.0	7 4	US-09-413-492-136	Sequence 136, App
19	18	60.0	8 3	US-07-961-307-2	Sequence 2, Appli
20	18	60.0	8 3	US-08-335-865J-16	Sequence 16, Appl
21	18	60.0	8 4	US-08-444-818-341	Sequence 341, App
22	18	60.0	8 4	US-08-444-818-342	Sequence 342, App
23	18	60.0	8 4	US-08-444-818-343	Sequence 343, App
24	18	60.0	8 4	US-08-444-818-344	Sequence 344, App
25	18	60.0	9 2	US-08-585-281-2	Sequence 2, Appli
26	18	60.0	9 2	US-08-585-281-3	Sequence 3, Appli
27	18	60.0	9 2	US-08-585-281-5	Sequence 5, Appli
28	18	60.0	9 2	US-08-585-281-6	Sequence 6, Appli
29	18	60.0	9 3	US-08-159-339A-619	Sequence 619, App
30	18	60.0	10 1	US-08-250-789A-94	Sequence 94, Appl
31	18	60.0	10 1	US-08-250-789A-95	Sequence 95, Appl
32	18	60.0	10 1	US-08-250-789A-96	Sequence 96, Appl
33	18	60.0	10 1	US-08-250-789A-97	Sequence 97, Appl
34	17	56.7	4 1	US-08-219-156-5	Sequence 5, Appli
35	17	56.7	4 1	US-08-238-089-5	Sequence 5, Appli
36	17	56.7	4 1	US-08-238-089-6	Sequence 6, Appli
37	17	56.7	4 1	US-08-366-783-8	Sequence 8, Appli
38	17	56.7	4 1	US-08-432-651A-5	Sequence 5, Appli
39	17	56.7	4 1	US-08-432-651A-6	Sequence 6, Appli
40	17	56.7	4 1	US-08-798-897-49	Sequence 49, Appl
41	17	56.7	4 2	US-08-707-237A-97	Sequence 97, Appl
42	17	56.7	4 2	US-08-978-523-49	Sequence 49, Appl
43	17	56.7	4 2	US-08-846-021A-11	Sequence 11, Appl
44	17	56.7	4 3	US-08-642-246-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-08-953-033-7

; Sequence 7, Application US/08953033

; Patent No. 6165977

; GENERAL INFORMATION:

; APPLICANT: Mochly-Rosen, Daria

; TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS

; TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM

; TITLE OF INVENTION: POSITIONS

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/953,033

; FILING DATE: 17-OCT-1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/028,724

; FILING DATE: 18-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Petithory, Joanne R.

; REGISTRATION NUMBER: 42,995

; REFERENCE/DOCKET NUMBER: 8600-0174.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-0880

; TELEFAX: 650-324-0960

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...8
; OTHER INFORMATION: epsilonV1-7.1
US-08-953-033-7

Query Match 70.0%; Score 21; DB 4; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLGXY 6
|:|
Db 4 PIGDY 8

Search completed: October 23, 2002, 13:43:30
Job time : 15 secs